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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/572,027DATE: 02/14/96
TIME: 17:56:58

INPUT SET: S8732.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERE

(1) General Information:

(i) APPLICANT: DeBonte, L. et al.

(ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER
ALTERED FATTY ACID PROFILES

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish & Richardson, P.C., P.A.
- (B) STREET: 60 South Sixth Street, Suite 3300
- (C) CITY: Minneapolis
- (D) STATE: MN
- (E) COUNTRY: USA
- (F) ZIP: 55402

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/416,497
- (B) FILING DATE: 04-APR-1995

- (A) APPLICATION NUMBER: US 08/170,886
- (B) FILING DATE: 21-DEC-1993

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/739,965
- (B) FILING DATE: 05-AUG-1991
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/575,542
- (B) FILING DATE: 30-AUG-1990

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TIME: 17:57:01

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47         (C) CLASSIFICATION:
48
49     (viii) ATTORNEY/AGENT INFORMATION:
50         (A) NAME: Ellinger, Mark S.
51         (B) REGISTRATION NUMBER: 34,812
52         (C) REFERENCE/DOCKET NUMBER: A21-535.10
53
54     (ix) TELECOMMUNICATION INFORMATION:
55         (A) TELEPHONE: 612/335-5070
56         (B) TELEFAX: 612/288-9696
57
58     (2) INFORMATION FOR SEQ ID NO:1:
59
60         (i) SEQUENCE CHARACTERISTICS:
61             (A) LENGTH: 1155 base pairs
62             (B) TYPE: nucleic acid
63             (C) STRANDEDNESS: single
64             (D) TOPOLOGY: linear
65
66         (ii) MOLECULE TYPE: DNA
67
68         (iii) HYPOTHETICAL: NO
69
70         (iv) ANTI-SENSE: NO
71
72         (vi) ORIGINAL SOURCE:
73             (A) ORGANISM: Brassica napus
74
75         (ix) FEATURE:
76             (D) OTHER INFORMATION: Wild type D form.
77
78
79         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
80
81     ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT      48
82     Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
83         1             5             10             15
84
85     GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT      96
86     Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
87         20             25             30
88
89     GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG     144
90     Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
91         35             40             45
92
93     ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC     192
94     Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
95         50             55             60
96
97     TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT     240
98     Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
99         65             70             75             80

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153  GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC      912
154  Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
155      290                      295                      300
156
157  TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT      960
158  Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
159  305                      310                      315                      320
160
161  CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG      1008
162  Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
163      325                      330                      335
164
165  ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG      1056
166  Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
167      340                      345                      350
168
169  GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG      1104
170  Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
171      355                      360                      365
172
173  GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T      1153
174  Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
175      370                      375                      380
176
177  GA      1155
178
179
180  (2) INFORMATION FOR SEQ ID NO:2:
181
182      (i) SEQUENCE CHARACTERISTICS:
183          (A) LENGTH: 384 amino acids
184          (B) TYPE: amino acid
185          (D) TOPOLOGY: linear
186
187      (ii) MOLECULE TYPE: protein
188
189      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
190
191  Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
192      1                      5                      10                      15
193
194  Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
195      20                      25                      30
196
197  Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
198      35                      40                      45
199
200  Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
201      50                      55                      60
202
203  Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
204      65                      70                      75                      80
205

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206 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
207           85                      90                      95
208
209 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
210           100                      105                      110
211
212 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
213           115                      120                      125
214
215 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
216           130                      135                      140
217
218 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
219           145                      150                      155                      160
220
221 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
222           165                      170                      175
223
224 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
225           180                      185                      190
226
227 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
228           195                      200                      205
229
230 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
231           210                      215                      220
232
233 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
234           225                      230                      235                      240
235
236 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
237           245                      250                      255
238
239 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
240           260                      265                      270
241
242 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
243           275                      280                      285
244
245 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
246           290                      295                      300
247
248 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
249           305                      310                      315                      320
250
251 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
252           325                      330                      335
253
254 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
255           340                      345                      350
256
257 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
258           355                      360                      365

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SEQUENCE VERIFICATION REPORT
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